

WHAT IS CLAIMED IS

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1. Oligonucleotide for the specific identification of *Staphylococci* species having a nucleotide sequence comprising between 15 and 350 base pairs, preferably between 17 and 250 base pairs, and which presents less than 50% homology with the "consensus" femA nucleotide sequence (CNS) of Fig. 3.

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2. Oligonucleotide according to claim 1 for the specific identification of *Staphylococci* species having a nucleotide sequence comprising between 15 and 350 base pairs, preferably between 17 and 250 base pairs, and which presents less than 40% homology with the "consensus" femA nucleotide sequence (CNS) of Fig. 3.

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3. Oligonucleotide according to claim 1 or 2 for the specific identification of *Staphylococci* species having a nucleotide sequence comprising between 15 and 350 base pairs, preferably between 17 and 250 base pairs, and which presents less than 30% homology with the "consensus" *femA* nucleotide sequence (CNS) of Fig. 3.

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4. Oligonucleotide according to any of the claims 1 to 3 for the specific identification of Staphylococci species having a nucleotide sequence comprising between 15 and 350 base pairs, preferably between 17 and 250 base pairs, and which presents less than 20% homology with the "consensus" femA nucleotide sequence (CNS) of Fig. 3.

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30 5. Oligonucleotide according to claim 1,
being a primer which nucleotide sequence has between 15 and
45 base pairs, preferably between 17 and 25 base pairs.

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6. Oligonucleotide according to claim 5,
which is selected from the group consisting of the
following nucleotide sequences :

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- ACAGCAGATGACATCATT
- TAATGAAAGAAATGTGCTTA
- ACACAACCTTCAATTAGAAC
- AGTATTAGCAAATGCGG
- 5 - ATGCATATTTTCCGTAA
- CAGCAGATGACATCATT
- CATCTAAAGATATATTAAATGGA
- AGTATTAGCAAATGCGGGTCAC
- CAACACAACCTTCAATTAGAA

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10 7. Couple of oligonucleotides for the specific amplification of *Staphylococci* species consisting of two different nucleotide sequences having between 15 and 45 base pairs, preferably between 17 and 25 base pairs, and which present more than 60% homology with the "consensus" femA nucleotide sequence (CNS) of Fig. 3 or consisting of

15 one nucleotide sequence having between 15 and 45 base pairs, preferably between 17 and 25 base pairs, and which presents more than 60% homology with the "consensus" femA nucleotide sequence (CNS) of Fig. 3 and the oligonucleotide

20 of claim 6.

8. Couple of oligonucleotides according to claim 7 for the specific amplification of *Staphylococci* species, consisting of two different nucleotide sequences having between 15 and 45 base pairs, preferably between 17

25 and 25 base pairs, and which present more than 70% homology with the "consensus" femA nucleotide sequence (CNS) of Fig. 3 or consisting of one nucleotide sequence having between 15 and 45 base pairs, preferably between 17 and 25 base pairs, and which presents more than 70% homology with

30 the "consensus" femA nucleotide sequence (CNS) of Fig. 3 and the oligonucleotide of claim 6.

9. Couple of oligonucleotides according to claim 7 or 8 for the specific amplification of *Staphylococci* species, consisting of two different

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nucleotide sequences having between 15 and 45 base pairs, preferably between 17 and 25 base pairs, and which present more than 80% homology with the "consensus" *femA* nucleotide sequence (CNS) of Fig. 3 or consisting of one nucleotide sequence having between 15 and 45 base pairs, preferably between 17 and 25 base pairs, and which presents more than 80% homology with the "consensus" *femA* nucleotide sequence (CNS) of Fig. 3 and the oligonucleotide of claim 6.

10. Couple of oligonucleotides according to any one of the claims 7 to 9 for the specific amplification of *Staphylococci* species, consisting of two different nucleotide sequences having between 15 and 45 base pairs, preferably between 17 and 25 base pairs, and which present more than 90% homology with the "consensus" *femA* nucleotide sequence (CNS) of Fig. 3 or consisting of one nucleotide sequence having between 15 and 45 base pairs, preferably between 17 and 25 base pairs, and which presents more than 90% homology with the "consensus" *femA* nucleotide sequence (CNS) of Fig. 3 and the oligonucleotide of claim 6.

11. Couple of oligonucleotide according to any one of the claims 7 to 10, wherein the oligonucleotides having between 15 and 45 base pairs, preferably between 17 and 25 base pairs, and which present more than 60, 70, 80 or 90% homology with the "consensus" *femA* nucleotide sequence (CNS) of Fig. 3 are selected from the group consisting of the following nucleotide sequences:

- ANAATGAANTTTACNAATTTNACNGCNANAGANTT
and more particularly TAATGAAGTTTACAAAATTT or
TAATGAAGTTTACNAAATTT
- 30 - ATGNCNNANAGNCATTTNACNCANA
and more particularly TGCCATATAGTCATTTACGC
- TAGTNGGNATNAANAANAANNATAANGANGTNATTGC
- GTNCCNGTNATGAAANTNTTNAANTANTTTTATTC
- AATGCNGGNNANGATTGG

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- GNAANNGNAANACNAAAAAAGTNNANAANAATGGNGTNAAAGT
and more particularly AAAAAGTTCAAAAAATGG and
AAAAAGTACAAAAAATGG
 - AAGANGANNTNCCNATNTTNGNTCATTNATGGANGATAC
 - 5 - TATATNNANTTTGATGANTA
 - AANGANATNGANAAANGNCCNGANAANAANAAAA
and more particularly AAAGATATTGAAAAACGA,
AAAGATATTGAAAAGAGACC, AAAGATATCGAGAAAGAC and
AAAGACATCGACAAGCGT.
 - 10 - ANCATGGNAANGAATTACCNAT
and more particularly GAACATGGTAATGAATTAC
 - AATCCNTNTGAAAGTNGTNTANTANGCNGGTGG
 - AGNTATGCNNTNCAATGGNNNATGATTAANTATGC
 - TTTANNGANGANGCNGAAGATGNNGGNGTNNNTNAANTTNAAAAA
 - 15 and more particularly TTTACTGAAGATGCTGAAGA
 - GTTGGNGANTTNNTNAAACC
and more particularly GTTGGTGACTTTATTAAACC
 - ATGAAATTTACAGAGTTAA
12. Oligonucleotide having between 15 and 45
base pairs, preferably between 17 and 25 base pairs,
which is selected from the group consisting of the
following nucleotide sequences:
- ANAATGAANTTTACNAATTTNACNGCNANAGANTT
and more particularly TAATGAAGTTTACAAAATTT or
 - 25 - TAATGAAGTTTACNAAATTT
 - ATGNCNNANAGNCATTTNACNGANA
and more particularly TGCCATATAGTCATTTACGC
 - TAGTNGGNATNAANAANANANNATAANGANGTNATTGC
 - GTNCCNGTNATGAAANTNTTNAANTANTTTTATTC
 - 30 - AATGCNGGNNANGATTGG
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- GNAANNNGNAANACNAAAAAAGTNNANAANAATGGNGTNAAAGT
and more particularly AAAAAGTTCAAAAAATGG and
AAAAAGTACAAAAAATGG
- AAGANGANNTNCCNATNTTNGNTCATTNATGCANGATAC
- 5 - TATATNNANTTTGATGANTA
- AANGANATNGANAAANGNCCNGANAANAANAAAA
and more particularly AAAGATATTGAAAAACGA,
AAAGATATTGAAAAGAGACC, AAAGATATCGAGAAAGAC and
AAAGACATCGACAAGCGT.
- 10 - ANCATGGNAANGAATTACCNAT
- AATCCNTNTGAAGTNGTNTANTANGCNGGTGG
- AGNTATGCNNTNCAATGCNNNATGATTAANTATGC
- TTTANNGANGANGCNGAAGATGNNGGNGTNNNTNAANTTNAAAAA
and more particularly TTTACTGAAGATGCTGAAGA
- 15 - GTTGGNGANTTNNTNAAACC
- and more particularly GTTGGTGACTTTATTAAACC
- ATGAAATTTACAGAGTTAA

13. Identification and/or quantification
method of a *Staphylococci* species, which may present
resistance to antibiotics and which is present in a
sample, said method comprising the steps of :

- 20 - obtaining a nucleotide sequence from a *Staphylococci*
species present in the sample,
- amplifying said nucleotide sequence with the couple of
oligonucleotides according to any one of the claims 7 to
11, and
- 25 - identifying and possibly quantifying the specific
Staphylococci species :

- 30 - by reverse hybridisation of the amplified
nucleotide sequence with one or more
oligonucleotide(s) according to any one of the
claims 1 to 6 which is (are) specific of said
Staphylococci species and is (are) immobilised on a
solid support or

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- by a comparative measure of the length of the amplified nucleotide sequence.

14. Diagnostic device for the identification of *Staphylococci* species comprising the oligonucleotide or the couple of oligonucleotides according to any one of the preceding claims 1 to 11 and possibly all the media necessary for the identification of an amplified sequence of said *Staphylococci* species through any one of the methods selected from the group consisting of in situ hybridisation, hybridisation on a solid support, in solution on dot blot, Northern blot, Southern blot, probe hybridisation by the use of an isotopic or non-isotopic label, genetic amplification or a mixture thereof.

15. *femA* genetic sequence which presents more than 90% homology with a nucleotide or amino acid sequence selected from the group consisting of the sequence SEQ ID NO 40, SEQ ID NO 41, SEQ ID NO 42, SEQ ID NO 43, SEQ ID NO 44, SEQ ID NO 45, SEQ ID NO 46, SEQ ID NO 47, SEQ ID NO 48, SEQ ID NO 49, SEQ ID NO 50, SEQ ID NO 51, SEQ ID NO 52, SEQ ID NO 53 and SEQ ID NO 54.

16. Genetic sequence according to claim 14, being the nucleotide sequence SEQ ID NO 40.

17. Genetic sequence according to claim 14, being the amino acid sequence SEQ ID NO 41.

25 18. Genetic sequence according to claim 14, being the nucleotide sequence SEQ ID NO 42.

19. Genetic sequence according to claim 14, being the amino acid sequence SEQ ID NO 43.

30 20. Genetic sequence according to claim 14, being the nucleotide sequence SEQ ID NO 44.

21. Genetic sequence according to claim 14, being the amino acid sequence SEQ ID NO 45.

22. Genetic sequence according to claim 14, being the nucleotide sequence SEQ ID NO 46.

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23. Genetic sequence according to claim 14,
being the amino acid sequence SEQ ID NO 47.

24. Genetic sequence according to claim 14,
being the nucleotide sequence SEQ ID NO 48.

5 25. Genetic sequence according to claim 14,
being the amino acid sequence SEQ ID NO 49.

26. Genetic sequence according to claim 14,
being the nucleotide sequence SEQ ID NO 50.

10 27. Genetic sequence according to claim 14,
being the amino acid sequence SEQ ID NO 51.

28. Genetic sequence according to claim 14,
being the nucleotide sequence SEQ ID NO 52.

29. Genetic sequence according to claim 14,
being the amino acid sequence SEQ ID NO 53.

15 30. Genetic sequence according to claim 14,
being the nucleotide sequence SEQ ID NO 54.

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